

## SEQUENCE LISTING

<110> Novak, Julia E.  
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<120> NOVEL CYTOKINE ZALPHA11 LIGAND

<130> 99-16

<150> US 60/123,547  
<151> 1999-03-09

<150> US 60/123,904  
<151> 1999-03-11

<150> US 60/142,013  
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aaraarytna armgnhaarcc nccnwsnacn aaygcnggnm gnmgnacraa rcaymgnytn	360
acntgyccnw sntgygayws ntaygaraar aarccnccna argarttyyt ngarmgnnty	420
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ccaaagagta ttagttctga gttggtgata caagtaaaaa ggctccttt gcattaatta	360
aaaaaaatatt atttaaattt cattgtgaca aacatggcct tccaagtca ttttcataga	420
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gat cct gaa ctt cta tca gct cca caa gat gta aag ggg cac tgt gag Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu	248
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	781

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gaaaactaaa gcttttagca aaaatacagc taggaaattt gtcgatctgc gagagtaaga	901
cctcttatga tcctaacgga atgatgtaag ctggaaataa taagcataag atgaaattga	961
aaattgaagt ctttattctt taagaaaaac ttgtacttg aaagcatgtc tgaagagttt	1021
actcattacc acaaacatct agcatattga taactaacat ctttatactc tacaagagag	1081
gctttccaga taggtacagt ttttcttc tattaggtct atcaaaaattt aacctattat	1141
gagggtcacc cctggcttc actgttttc taaagaggca agggtgttgt aagaagcagg	1201
cctaagttgc cttcctccca atgtcaagtt cctttataag ctaatagtt aatcttgta	1261
agatggcaat gaaagcctgt ggaagtgc当地 acctcactat cttctggagc caagtagaat	1321
tttcaagttt gtagctctca cctcaagtgg ttatgggtgt cctgtatgtc atctgctagc	1381
tccagcctca gtctcctc ccacatcctt tcctttctt cctcttggaa acttctaaga	1441
aaaagcaatc caaacaagtt cagcacttaa gacacattgc atgcacactt ttgataagtt	1501
aaatccaaacc atctatttaa aatcaaaaatc aggagatgag ccaagagacc agaggtctg	1561
ttccagttt aaacagactt ttactgaaca tcccaatctt ttaaccacag aggctaaatt	1621
gagcaaatacg tttgccatt tgatataatt tccaacagta tgttcaatg tcaagttaaa	1681
aagtctacaa agctatttc cctggagtgg tatcatcgct ttgagaattt cttatggta	1741
aaatggatct gagatccaag catggctgg gggatggttt tgatctaagg aaaaaggtgt	1801
ctgtacctca cagtgcctt aaaacaagca gagatcccgt gtaccgcct aagatagcac	1861
agactagtgt taactgattc ccagaaaagt gtcacaatca gaaccaacgc attctttaa	1921
actttaaaaa tatgtattgc aaagaacttg ttaactgtt aatgtgtgac tttgtatgac	1981
attatacaca catagccac gtaagtgtcc aatggtgcta gcattggttt ctgagttgc	2041
tgctcgaaag ctgaagcaga gatgcagtcc ttccacaaagc aatgtatggac agagagggga	2101
gtctccatgt tttattctt tttgtttctt ggctgtgtaa ctgttgactt cttgacattt	2161
tgattttat attaaagaca atgtattttt ttgggtgtgt ttattttctt agcctttaa	2221
atcaactgaca atttctaatac aagaagtaca aataattcaa tgcagcacag gctaagagct	2281
tgtatcggtt gaaaaagcca gtgaaggctt ctccactagc catggaaag ctacgcttta	2341
gagtaaacta gacaaaattt cacagcagtc ttgaacctct ctgtgtcaa gactcagcca	2401
gtccttgcattt attattgttc actgtgggtt ggaacacatt ggacctgaca cactgtgt	2461
tgtccatgaa ggttgcact ggttaagct tttttgggtt ttcatctct tatctgtaga	2521
acaagaatgt ggggcttcc taagtctatt ctgtattttt ttctgaactt cgtatgtctg	2581
agttttatgt ttttgagtac tcttacagga acacctgacc acactttga tttaaattttt	2641
atcccaagtgt tgatatttag ttgttcaaaa agggaaaggga tatacataca tacatacata	2701
catacataca tatatatata tatatatata tatatatata tatatatatg tatatatata	2761
tatatataga gagagagaga gagagagaga gagaaagaga gagaggttgt ttaggtcat	2821
aggagttcag agaaaatcag ttatggccgt taataactgtt gctgaaagtgt tttttttgt	2881
gaataaatttca atagcattat tgatctatgt tattgtctg ttttatttttac agtcacac	2941
gagaatttag ttttaatatgt aatgtatgtac ttatataactt aatgatttatt tattatgtat	3001
ttggtttga atttttgtgt tcatggcttc ttatataaga cctgtatcata tttaatgtca	3061
cccaagtccgg a	3072

&lt;210&gt; 56

&lt;211&gt; 146

&lt;212&gt; PRT

<213> mus musculus

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 1 5 10 15  
 Ala His Lys Ser Ser Pro Gln Gly Pro Asp Arg Leu Leu Ile Arg Leu  
 20 25 30  
 Arg His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp  
 35 40 45  
 Leu Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys  
 50 55 60  
 Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser  
 65 70 75 80  
 Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu  
 85 90 95  
 Arg Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile  
 100 105 110  
 Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu  
 115 120 125  
 Phe Leu Glu Arg Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His  
 130 135 140  
 Leu Ser  
 145

<210> 57  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22283

<400> 57  
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34

<210> 58  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22284

<400> 58  
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<210> 59  
 <211> 100  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC12749

<400> 59  
 gtacctccct gtaaatccct cccctccccg gaattacaca cgcttatttc ccagaaaagg 60  
 aactgttagat ttcttaggaat tcaatccttg gccacgcgtc 100

<210> 60  
 <211> 100  
 <212> DNA  
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<220>  
 <223> Oligonucleotide ZC12748

<400> 60  
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 cgcgtgtgtt attccggaa ggggagggat ttacggaaag 100

<210> 61  
 <211> 32  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC22143

<400> 61  
 cgtatcgccc ggccaccatg agatccagtc ct 32

<210> 62  
 <211> 32  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC22144

<400> 62  
 cgtacggcg cgccctcagga atttcactt cc 32

<210> 63  
 <211> 483  
 <212> DNA  
 <213> homo sapiens

<400> 63  
 tccagtcctg gcaacatgga gaggattgtc atctgtctga tggtcatctt cttggggaca 60  
 ctggccaca aatcaagctc ccaaggtaa gatgccaca tgattagaat gctcaactt 120  
 atagatattt tgatcagct gaaaaattat gtgaatgact tggtccctga atttctgcca 180  
 gctccagaag atgttagagac aaactgtgag tggtcagctt tttcctgtt tcagaaggcc 240  
 caactaaagt cagcaaatac aggaaacaat gaaaggataa tcaatgtatc aattaaaaag 300  
 ctgaagagga aaccaccttc cacaatgca gggagaagac agaaacacag actaacatgc 360  
 cttcatgtg attcttatga gaaaaaaccat cccaaagaat tccttagaaag attcaaatac 420  
 cttctccaaa agatgattca tcagcatctg tcctctagaa cacacggaag tgaagattcc 480  
 tga 483

<210> 64  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22052

<400> 64  
 tcatataggc cgccatatacg cccggcgcc accatggatt ccagtctgg caacatg 57

<210> 65  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22053

<400> 65  
 gtacaacccc agagctgttt taaggcgcbc ctcttagatca ggaatcttca cttccgt 57

<210> 66  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC23115

<400> 66  
gtatacggcc ggccaccatg gagaggaccc tt 32

<210> 67  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC23116

<400> 67  
cgtatcggcg cgccctagga gagatgctga tg 32

<210> 68  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC20892

<400> 68  
gtatacgttt aaacgccacc atgccgcgtg gctgg 35

<210> 69  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC20893

<400> 69

cgtatcggcg cgccttacaa tggatgggtc tt	32
<210> 70	
<211> 39	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Oligonucleotide primer ZC22054	
<400> 70	
cccggggtcg acaccatgga ttccagtcct ggcaacatg	39
<210> 71	
<211> 32	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Oligonucleotide primer ZC22055	
<400> 71	
tgcagttaa actcaggaat cttcacttcc gt	32
<210> 72	
<211> 40	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Huzalphal1L-1 peptide	
<400> 72	
Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp	
1 5 10 15	
Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala	
20 25 30	
Pro Glu Asp Val Glu Thr Asn Cys	
35 40	
<210> 73	
<211> 32	
<212> PRT	

<213> Artificial Sequence

<220>

<223> Huzalpha11L-3 peptide

<400> 73

Cys Pro Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu  
1 5 10 15

Glu Arg Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser  
20 25 30

<210> 74

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23444

<400> 74

gccccgggcgg atccatggat tccagtcct 29

<210> 75

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23445

<400> 75

cgcgccctcg agtcaggaat cttcacttcc gt 32

<210> 76

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC447

<400> 76

taacaatttc acacagg 17

<210> 77		
<211> 18		
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<220>		
<223> Oligonucleotide primer ZC976		
<400> 77		
cgttgtaaaa cgacggcc	18	
<210> 78		
<211> 66		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Oligonucleotide primer ZC22128		
<400> 78		
tcaccacgcg aattcggtag cgcgtggatcc caagatcgcc acatgattag	60	
aatgcg	66	
<210> 79		
<211> 68		
<212> DNA		
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<223> Oligonucleotide primer ZC22127		
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tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca tcaggaatct tcacttccgt	60	
gtgttcta	68	
<210> 80		
<211> 40		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Oligonucleotide primer ZC19372		

<400> 80  
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<210> 81  
<211> 60  
<212> DNA  
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<220>  
<223> Oligonucleotide primer ZC19351

<400> 81  
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<210> 82  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC19352

<400> 82  
actcaCTATA gggcgaattg cccggggat ccacgcggaa ccAGCGGTAC cgaattcgCG 60

<210> 83  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC19371

<400> 83  
acggccAGTG aattgtata CGACTCACTA tagggcGAAT TG 42

<210> 84  
<211> 1560  
<212> DNA  
<213> Artificial Sequence

<220>

&lt;221&gt; CDS

&lt;222&gt; (1)...(1560)

&lt;223&gt; MBP-human zalpha1I Ligand fusion polynucleotide

<400> 84				
atg aaa act gaa gaa ggt aaa ctg gta atc tgg att aac ggc gat aaa				48
Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys				
1 5 10 15				
ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc				96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr				
20 25 30				
gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc				144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe				
35 40 45				
cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca				192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala				
50 55 60				
cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc				240
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile				
65 70 75 80				
acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat				288
Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp				
85 90 95				
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa				336
Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu				
100 105 110				
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa				384
Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys				
115 120 125				
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt				432
Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly				
130 135 140				



acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln	325	330	335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala	340	345	350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn	355	360	365	1104
tcg agc tcc cac cat cac cat cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His Ala Asn Ser Val Pro Leu Val	370	375	380	1152
ccg cgt gga tcc caa gat cgc cac atg att aga atg cgt caa ctt ata Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile	385	390	395	400
gat att gtt gat cag ctg aaa aat tat gtg aat gac ttg gtc cct gaa Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu	405	410	415	1248
ttt ctg cca gct cca gaa gat gta gag aca aac tgt gag tgg tca gct Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala	420	425	430	1296
ttt tcc tgt ttt cag aag gcc caa cta aag tca gca aat aca gga aac Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn	435	440	445	1344
aat gaa agg ata atc aat gta tca att aaa aag ctg aag agg aaa cca Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro	450	455	460	1392
cct tcc aca aat gca ggg aga aga cag aaa cac aga cta aca tgc cct Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro	465	470	475	1440
			480	

ttc aaa tca ctt ctc caa aag atg att cat cag cat ctg tcc tct aga 1536  
Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg  
500 505 510

aca cac gga agt gaa gat tcc tga 1560  
Thr His Gly Ser Glu Asp Ser \*  
515

<210> 85  
<211> 519  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> MBP-human zalpha1I Ligand fusion polypeptide

<400> 85  
 Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys  
 1 5 10 15  
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr  
 20 25 30  
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe  
 35 40 45  
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala  
 50 55 60  
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile  
 65 70 75 80  
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp  
 85 90 95  
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu  
 100 105 110  
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys  
 115 120 125  
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly  
 130 135 140  
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro  
 145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys  
                  165                 170                 175  
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly  
                  180                 185                 190  
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp  
                  195                 200                 205  
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala  
                  210                 215                 220  
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
                  225                 230                 235                 240  
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser  
                  245                 250                 255  
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
                  260                 265                 270  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
                  275                 280                 285  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
                  290                 295                 300  
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
                  305                 310                 315                 320  
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
                  325                 330                 335  
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala  
                  340                 345                 350  
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn  
                  355                 360                 365  
 Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val  
                  370                 375                 380  
 Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile  
                  385                 390                 395                 400  
 Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu  
                  405                 410                 415  
 Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala  
                  420                 425                 430  
 Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn  
                  435                 440                 445  
 Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro  
                  450                 455                 460  
 Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro  
                  465                 470                 475                 480  
 Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg  
                  485                 490                 495

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg  
 500 505 510

Thr His Gly Ser Glu Asp Ser  
 515

<210> 86  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22849

<400> 86  
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 actt 64

<210> 87  
 <211> 64  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC22850

<400> 87  
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 tcat 64

<210> 88  
 <211> 1533  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> MBP-mouse zalpha1I Ligand fusion polynucleotide

<221> CDS  
 <222> (1)...(1533)

<400> 88

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1 5 10 15	
ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr	96
20 25 30	
gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe	144
35 40 45	
cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala	192
50 55 60	
cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile	240
65 70 75 80	
acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp	288
85 90 95	
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu	336
100 105 110	
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys	384
115 120 125	
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly	432
130 135 140	
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro	480
145 150 155 160	
ctg att gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys	528
165 170 175	

tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt  
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly  
 180 185 190 576

ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac  
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp  
 195 200 205 624

acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gca gct  
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala  
 210 215 220 672

atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa  
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
 225 230 235 240 720

gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc  
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser  
 245 250 255 768

aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg  
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
 260 265 270 816

aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
 275 280 285 864

gaa ggt ctg gaa ggc gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
 290 295 300 912

ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc  
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
 305 310 315 320 960

acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag  
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
 325 330 335 1008

atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala	340	345	350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn	355	360	365	1104
tcg agc tcc cac cat cac cat cac gcg aat tcg gta ccg ctg gtt Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val	370	375	380	1152
ccg cgt gga tcc cca gat cgc ctc ctg att aga ctt cgt cac ctt att Pro Arg Gly Ser Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile	385	390	395	1200
gac att gtt gaa cag ctg aaa atc tat gaa aat gac ttg gat cct gaa Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu	405	410	415	1248
ctt cta tca gct cca caa gat gta aag ggg cac tgt gag cat gca gct Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala	420	425	430	1296
ttt gcc tgt ttt cag aag gcc aaa ctc aag cca tca aac cct gga aac Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn Pro Gly Asn	435	440	445	1344
aat aag aca ttc atc att gac ctc gtg gcc cag ctc agg agg agg ctg Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu	450	455	460	1392
cct gcc agg agg gga aag aaa cag aag cac ata gct aaa tgc cct Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro	465	470	475	1440
tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc cta gaa aga Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg	485	490	495	1488
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<400> 89

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Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe
				35				40							45
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala
				50			55								60
His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile
				65			70				75				80
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp
					85				90						95
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu
				100				105							110
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys
				115				120							125
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly
				130			135				140				
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro
				145			150				155				160
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys
					165			170				175			
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly
					180			185				190			
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp
				195			200				205				
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala
				210			215				220				
Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys
				225			230				235				240
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser
				245			250				255				

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
                  260                     265                     270  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
                  275                     280                     285  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
                  290                     295                     300  
 Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
                  305                     310                     315                     320  
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
                  325                     330                     335  
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala  
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 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn  
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 Ser Ser Ser His His His His Asn Ser Val Pro Leu Val  
                  370                     375                     380  
 Pro Arg Gly Ser Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile  
                  385                     390                     395                     400  
 Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu  
                  405                     410                     415  
 Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala  
                  420                     425                     430  
 Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn Pro Gly Asn  
                  435                     440                     445  
 Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu  
                  450                     455                     460  
 Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro  
                  465                     470                     475                     480  
 Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg  
                  485                     490                     495  
 Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His Leu Ser  
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<400> 90

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ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc	96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr	
20               25               30	
gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc	144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe	
35               40               45	
cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca	192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala	
50               55               60	

cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc 240  
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile  
 65 70 75 80  
  
 acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat 288  
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp  
 85 90 95  
  
 gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa 336  
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu  
 100 105 110  
  
 gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa 384  
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys  
 115 120 125  
  
 acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt 432  
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly  
 130 135 140  
  
 aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg 480  
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro  
 145 150 155 160  
  
 ctg att gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag 528  
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys  
 165 170 175  
  
 tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt 576  
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly  
 180 185 190  
  
 ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac 624  
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp  
 195 200 205  
  
 acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg 672  
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala  
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 atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa 720  
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
 225 230 235 240

gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser	245	250	255	768
aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro	260	265	270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp	275	280	285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala	290	295	300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala	305	310	315	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln	325	330	335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala	340	345	350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn	355	360	365	1104
tcg agc tcc cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His Ala Asn Ser Val Pro Leu Val	370	375	380	1152
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln	385	390	395	1200
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu	405	410	415	1248

acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr 420	425	430	1296
tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr 435	440	445	1344
acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser 450	455	460	1392
gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser 465	470	475	480
ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr 485	490	495	1488
gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu 500	505	510	1536
gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln 515	520	525	1584
tac agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu 530	535	540	1632
atc tca gtg gac tca aga agt gtc tcc ctc ccc ctg gag ttc cgc Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg 545	550	555	560
aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly 565	570	575	1728
tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe 580	585	590	1776

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Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His *	
595	600
	605

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Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe			
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Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala			
50	55		60
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile			
65	70		75
Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp			
85	90		95
Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu			
100	105		110
Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys			
115	120		125
Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly			
130	135		140
Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro			
145	150		155
Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys			
165	170		175
Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly			
180	185		190
Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp			
195	200		205
Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala			
210	215		220

Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
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 245 250 255  
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
 260 265 270  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
 275 280 285  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
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 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
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 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
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 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala  
 340 345 350  
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn  
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 Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val  
 370 375 380  
 Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln  
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 Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu  
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 Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr  
 435 440 445  
 Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser  
 450 455 460  
 Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser  
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 Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr  
 485 490 495  
 Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu  
 500 505 510  
 Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln  
 515 520 525  
 Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu  
 530 535 540  
 Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg  
 545 550 555 560

Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly  
 565 570 575

Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe  
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Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His  
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aaaaaaagagt	tactcacatt	catccattt	acaaagattt	ccaggttgca	atgggagggc	180
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aacaaatttt	cttttgctct	aggtccctga	atttctgcca	gctccagaag	atgtagaggt	600
aagaccagtt	gaattttattt	ctgaaaatac	attggacata	agttttaaa	tccaataaga	660
aagacattag	catgattata	taggagtata	ctgaatttta	atgaacttag	cggctctaata	720
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aaaatgtat	attatattcc	tcataaaacta	tgtttatctt	caagaatctc	taagagtact	840
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gttttagaaa	agtcatggtg	tgtatctatgg	caagtatatt	gattcttaga	tgtaaaatat	120
gctatcagag	ggaggtaccc	acttccttc	tccaaaggag	gggcttaat	tcattttctt	180
catctgttaa	ctttacaaat	atatgttcat	cattaactgg	caagacacta	tgcctggcgc	240
tgtacagaat	aaaatgtgc	tcaagacatg	tcatgtatga	tacattaaca	gaaaccacaa	300
acaaatgaaa	aatgttcttc	atcagactat	aacataattt	acccaaagct	gccactagtc	360
acagtgtaa	tttagagcc	tcataactca	gcaaatgtgt	cctaaaccga	actaactctc	420

ctttataaaa cacaaggc ttgtccacca cccagacatc aaaatggcc tctgtgtac	480
atcaggaata aagcattgtg aagaagttag gtcctttct ctcttatctg cgaaggcagg	540
gattgtccct tttcccatc ccaaagatta agtaggaggt gaaatcatac ctcactcatc	600
tgttgaaacg atgtaatgca cgacattgca gaagagatag aaatagagga ttggaaagc	660
tatctttac ttctgaata atgttgtta acatatacac aaattgttta tcttcagac	720
aaactgtgag tggtcagctt ttccctgttt tcagaaggcc caactaaagt cagcaaatac	780
aggaaacaat gaaaggataa taaatgtatc aattaaaaag ctgaagagga aaccaccc	840
cacaaatgca gggagaagac agaaacacag actagtaaga ttgtcatttg tcatctct	900
tatgttact tataaactat atatctgca ttacataaac atacacacac acctgtagcc	960
agggctgctg gtgtcttcct tacctatagt tatgccttat tatacatggt gcttttttt	1020
tttaagacag agtctcaactc tgtcacccag gctggagtgc agtggcgtga tctctgtca	1080
ccgcaagatc cacctcccg tttcacgcca ttctcctcct acctcagcct cctgagtacc	1140
tggactaca ggtgccgccc accatccccg gctaattttg ttttgtatt tttagtaaag	1200
acagggttcc accatgttag ccaggatggt ctcgatctcc tgacccgtg atccgcccgc	1260
cttggcctcc caaagtgtgg ggattacagg catgagccac cgccacccggc ctatacgtgg	1320
tgcattttaa gaagtagggc cactcttttta agcccacaga cttgaaagta ttcaaaaacc	1380
caattataat ttccctagtag tccttggcag ctggaatatg ttaatatacg ttctcaaggt	1440
gaggaagtca ttaggcagag aatccaaactg tgattttgga gttaaagaact atttcctctc	1500
atatggtcac agataactt tattcttatt aacaggagct agatcctagc tttctaacaa	1560
gaaaagagcc tacaagaaga cttagggcaaa tcttaaactt tgcctcctct ctaaatcata	1620
ttactatctq tacatcaqca qaqtcqatq tqaatt	1656

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<212> DNA  
<213> *Homo sapiens*

<400> 107	
agctaaactt agaactctcc agttaagcat gttcatctta tagatgagga aaagtgagat	60
ctacaaagga gttaagtcac tagccccaaag ttccataaaat agtgtcagaa tgagaattag	120
aacgtatatac tactatcttt tagtgaardt ctctcaaac aacatcacac tggcatttag	180
atgctaacta ccaagcaatg gcttgggtt tggatctaaa tagggataaa gacaaagagc	240
ataaaactaag aaagctttt aaaaatctaa gtgagcaatc catatatgaa aaactgttca	300
atctccctag taatcacata aatgcgagtt aaaacaagga aatcctgttt tttccaatta	360
aacattttaa acaataaccct ataataataa gaatgctcca agtggaaaga ggtaaaaccc	420
tttataatgt atatcaaagc cttaaaaattt ttatccctt aatttagtaa ttctacttct	480
aggaatatat caaataagca aagatataata tgaaaaattt tttacagaga tgttcttgg	540
agtaatgttag acaaaaataa aaagtttagat acagctgggt gtggtggtc atgcctgtat	600
tcccaqcaact ttqqqaqqcc qaggcaggcg gatcacctga gatc	644

<210> 108  
<211> 645  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(645)

<223> n = A,T,C or G

<400> 108

aaaaaaaaaaa aaaaaaaaaaa gttagatgca ccnttgggtc caaaaatagt aagagtgcatt	60
cctatgtgga aacagaccaa ccactacatg tcataatttt gaagattatt taacacttag	120
gaaatcctgt gatatgttaa gtgtaaaaaa aaaaaagcaa atcaccact ggtataaata	180
atgtaaatgc acaataataa ttaaaaatac cccaaacaca gagagaatat acattaaaac	240
attgcagtgg gattcctatc tctggaaatg ggattacaag gacttttcc attgttactt	300
tccaaacagt tttatgtact tctcgaatgt tttcagtga acataattt aatgtttttaat	360
aaaaaaaaaat tttaagaaac attttattac gaaaaaaaaatt ttaaagaaga ctgttacttt	420
ttcattgatt tctagacatg cccttcatgt gattcttatg agaaaaaacc acccaaagaa	480
ttccttagaaa gattcaaatac acttctccaa aaggtatcta ccttaagttt catttgattt	540
tctgctttat ctttacctat ccagattgc ttcttagtta ctcacggat actattcca	600
cagatgattc atcagcatct gtcctctaga acacacggaa gtgaa	645

<210> 109

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC25970

<400> 109

atgcattcta gactaggaga gatgctgatg aatcat

36

<210> 110

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC25969

<400> 110

atgcattccg gacataaatac aagcccccaa gggcca

36

<210> 111

<211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 111

Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu
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Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	
				20				25						30	
Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile
				35				40						45	
Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Phe	Lys	Phe
				50				55						60	
Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu
				65				70						80	
Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala	Gln	Ser	Lys
				85				90						95	
Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile
				100				105						110	
Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala
				115				120						125	
Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe
				130				135						140	
Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr							
				145				150							

<210> 112  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 112

Met	Gly	Leu	Thr	Ser	Gln	Leu	Leu	Pro	Pro	Leu	Phe	Phe	Leu	Leu	Ala
1					5					10					15
Cys	Ala	Gly	Asn	Phe	Val	His	Gly	His	Lys	Cys	Asp	Ile	Thr	Leu	Gln
					20				25					30	
Glu	Ile	Ile	Lys	Thr	Leu	Asn	Ser	Leu	Thr	Glu	Gln	Lys	Thr	Leu	Cys
					35				40					45	
Thr	Glu	Leu	Thr	Val	Thr	Asp	Ile	Phe	Ala	Ala	Ser	Lys	Asn	Thr	Thr
					50				55					60	
Glu	Lys	Glu	Thr	Phe	Cys	Arg	Ala	Ala	Thr	Val	Leu	Arg	Gln	Phe	Tyr
					65				70					80	

Ser His His Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln  
                   85                  90                  95  
 Phe His Arg His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg  
                   100              105              110  
 Asn Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala  
                   115              120              125  
 Asn Gln Ser Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met  
                   130              135              140  
 Arg Glu Lys Tyr Ser Lys Cys Ser Ser  
                   145              150

<210> 113  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens

<400> 113  
 Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr  
   1              5                  10                  15  
 Leu Cys Leu Leu Leu Asn Ser His Phe Leu Thr Glu Ala Gly Ile His  
   20              25                  30  
 Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala  
   35              40                  45  
 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Ile Glu Asp Leu Ile  
   50              55              60  
 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His  
   65              70              75                  80  
 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
   85              90                  95  
 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
   100            105              110  
 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
   115            120              125  
 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
   130            135              140  
 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
   145            150              155                  160  
 Thr Ser

<210> 114  
 <211> 144  
 <212> PRT

<213> Homo sapiens

<400> 114

Met	Trp	Leu	Gln	Ser	Leu	Leu	Leu	Gly	Thr	Val	Ala	Cys	Ser	Ile	
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Ser	Ala	Pro	Ala	Arg	Ser	Pro	Ser	Pro	Ser	Thr	Gln	Pro	Trp	Glu	His
				20					25					30	
Val	Asn	Ala	Ile	Gln	Glu	Ala	Arg	Arg	Leu	Leu	Asn	Leu	Ser	Arg	Asp
				35				40					45		
Thr	Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser	Glu	Met	Phe
				50			55					60			
Asp	Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	Leu	Tyr	Lys
				65			70			75				80	
Gln	Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	Leu	Thr	Met
				85				90					95		
Met	Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Ser
				100				105					110		
Cys	Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	Asn	Leu	Lys
				115			120					125			
Asp	Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro	Val	Gln	Glu
				130			135					140			

<210> 115

<211> 538

<212> PRT

<213> Homo sapiens

<400> 115

Met	Pro	Arg	Gly	Trp	Ala	Ala	Pro	Leu	Leu	Leu	Leu	Leu	Gln	Gly	
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Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr
			20					25					30		
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr
			35				40					45			
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser
			50			55				60					
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr
			65			70			75				80		
Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val
				85				90					95		
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe
			100					105					110		

Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val  
           115                  120                  125  
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp  
           130                  135                  140  
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr  
           145                  150                  155                  160  
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile  
           165                  170                  175  
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys  
           180                  185                  190  
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser  
           195                  200                  205  
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln  
           210                  215                  220  
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu  
           225                  230                  235                  240  
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys  
           245                  250                  255  
 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser  
           260                  265                  270  
 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe  
           275                  280                  285  
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly  
           290                  295                  300  
 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His  
           305                  310                  315                  320  
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu  
           325                  330                  335  
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp  
           340                  345                  350  
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp  
           355                  360                  365  
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala  
           370                  375                  380  
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro  
           385                  390                  395                  400  
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp  
           405                  410                  415  
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser  
           420                  425                  430  
 Ala Gly Ser Pro Gly Leu Gly Pro Leu Gly Ser Leu Leu Asp Arg  
           435                  440                  445

Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro  
450 455 460  
Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser  
465 470 475 480  
Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly  
485 490 495  
Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp  
500 505 510  
Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro  
515 520 525  
Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser  
530 535